

1/12

SEQUENCE LISTING

<110> Scherer, Stephen W.

Minassian, Berge A.

<120> Lafora's Disease Gene

<130> 4012.1000-003

<150> PCT/CA2004/001449

<151> 2004-07-30

<150> US 60/491,968

<151> 2003-08-04

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 2120

<212> DNA

<213> Homo sapiens

```
<400> 1
atggcgggccg aagcctcgga gagcgggcca gcgctgcatg agctcatgcg cgaggcggag      60
atcagcctgc tcgagtgcaa ggtgtgcttt gagaagtttg gccaccggca gcagcggcgc      120
ccgcgcaacc tgtcctgcgg ccacgtggtc tgcctggcct gcgtggccgc cctggcgcac      180
ccgcgcactc tggccctcga gtgcccattc tgcaggcgag cttgccgggg ctgcgacacc      240
agcgactgcc tgccggtgct gcacctcata gagctcctgg gctcagcgct tcgccagtcc      300
ccggccgccc atcgcgccgc cccagcgcc cccggagccc tcacctgcca ccacaccttc      360
ggcgggctggg ggaccctggt caacccacc ggactggcgc tttgtcccaa gacggggcgt      420
```

gtcgtggtgg tgcacgacgg caggaggcgt gtcaagattt ttgactcagg gggaggatgc 480
 gcgcatcagt ttggagagaa gggggacgct gccaagaca ttaggtaccc tgtggatgtc 540
 accatcacca acgactgcc a tgtggttgtc actgacgccg gcgatcgctc catcaaagt 600
 tttgattttt ttggccagat caagcttgtc attggaggcc aattctcctt accttgggg 660
 gtggagacca cccctcagaa tgggattgtg gtaactgatg cggaggcagg gtccctgcac 720
 ctctggacg tcgacttcgc ggaaggggtc cttcgagaa ctgaaagggt gcaagctcat 780
 ctgtgcaatc cccgaggggt ggcatgtct tggctcaccg gggccattgc ggtctggag 840
 cccccctgg ccctggggac tggggtttgc agcaccaggg tgaaagtgt tagctcaagt 900
 atgcagcttg tcggccaagt ggatacctt gggctgagcc tctactttcc ctccaaaata 960
 actgcctccg ctgtgacct tgatcaccag ggaaatgtga ttgttgaga tacatctggt 1020
 ccagctatcc tttgcttagg aaaacctgag gagtttccag taccgaagcc catggctact 1080
 catggtcttt cgcactctgt ggctcttacc ttcaccaagg agaattctct tcttgtgctg 1140
 gacacagcat ctcatctat aaaagtctat aaagttgact gggggtgatg ggctgggggtg 1200
 ggtccctgga atcagaagca ctagtgctgc cattaatgaa ttgtttaacc ctggataagt 1260
 cacttaaact catctatcca ggcagggata attaaaacca tctggcagac ttacaaagct 1320
 tgggacagtt attggagatt aatctacat ttattgaatg catactctgt gcaaggaaat 1380
 ttgcaaatat tagcttattt aatctgtact atccagtgag gtaatttctt ccccccaag 1440
 atagagtcaa gctctgtcac ccaggctgga gtgcagaagc atgatcacag ctactacag 1500
 tttcaacgtc ccccgctcag gtggctcttc cacctcagcc tccaagtag ctgggaccac 1560
 aagtgtgcat taccacactc agctaatttt tgtattttgg cagagatggg gtttcacat 1620
 gttgccagg ctggtctcaa actcctgagt tcaagcaatc caccttcctc ggctcccaa 1680
 agtactagga gtacaggcat agccacttgc tcagccataa tttttattat taatctcatt 1740
 gtacaagtga gaaaactgag acccagagag cttaagtgc ttcctcgagg tcatagttac 1800
 ttactgcctt agtcccaatt tgaattcaat tctgattcca aataagttgc gcttaataa 1860
 gacaacagat gtgggaaaaa tatgtgaatg tgtagtggtg ctatgtgtac tgtctttaca 1920
 agtagctaata ttttttagca caaagatgtg caaagaaagg agactttatg gagagttcag 1980
 gagaaaaagg attttgtggt ggccatcact ttcattcaat ttgcgactgc tctgatggca 2040
 cattagatga agttactgtt gatcctgagt tacgtgaata agaaaaaca ttgaactgct 2100
 tattaataaaa gtaaacaatgt 2120

<210> 2

<211> 395

3/12

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ala Glu Ala Ser Glu Ser Gly Pro Ala Leu His Glu Leu Met
 1 5 10 15

Arg Glu Ala Glu Ile Ser Leu Leu Glu Cys Lys Val Cys Phe Glu Lys
 20 25 30

Phe Gly His Arg Gln Gln Arg Arg Pro Arg Asn Leu Ser Cys Gly His
 35 40 45

Val Val Cys Leu Ala Cys Val Ala Ala Leu Ala His Pro Arg Thr Leu
 50 55 60

Ala Leu Glu Cys Pro Phe Cys Arg Arg Ala Cys Arg Gly Cys Asp Thr
 65 70 75 80

Ser Asp Cys Leu Pro Val Leu His Leu Ile Glu Leu Leu Gly Ser Ala
 85 90 95

Leu Arg Gln Ser Pro Ala Ala His Arg Ala Ala Pro Ser Ala Pro Gly
 100 105 110

Ala Leu Thr Cys His His Thr Phe Gly Gly Trp Gly Thr Leu Val Asn
 115 120 125

Pro Thr Gly Leu Ala Leu Cys Pro Lys Thr Gly Arg Val Val Val Val
 130 135 140

His Asp Gly Arg Arg Arg Val Lys Ile Phe Asp Ser Gly Gly Gly Cys
 145 150 155 160

Ala His Gln Phe Gly Glu Lys Gly Asp Ala Ala Gln Asp Ile Arg Tyr
 165 170 175

Pro Val Asp Val Thr Ile Thr Asn Asp Cys His Val Val Val Thr Asp
 180 185 190

Ala Gly Asp Arg Ser Ile Lys Val Phe Asp Phe Phe Gly Gln Ile Lys
 195 200 205

Leu Val Ile Gly Gly Gln Phe Ser Leu Pro Trp Gly Val Glu Thr Thr
 210 215 220

4/12

Pro Gln Asn Gly Ile Val Val Thr Asp Ala Glu Ala Gly Ser Leu His
 225 230 235 240

Leu Leu Asp Val Asp Phe Ala Glu Gly Val Leu Arg Arg Thr Glu Arg
 245 250 255

Leu Gln Ala His Leu Cys Asn Pro Arg Gly Val Ala Val Ser Trp Leu
 260 265 270

Thr Gly Ala Ile Ala Val Leu Glu His Pro Leu Ala Leu Gly Thr Gly
 275 280 285

Val Cys Ser Thr Arg Val Lys Val Phe Ser Ser Ser Met Gln Leu Val
 290 295 300

Gly Gln Val Asp Thr Phe Gly Leu Ser Leu Tyr Phe Pro Ser Lys Ile
 305 310 315 320

Thr Ala Ser Ala Val Thr Phe Asp His Gln Gly Asn Val Ile Val Ala
 325 330 335

Asp Thr Ser Gly Pro Ala Ile Leu Cys Leu Gly Lys Pro Glu Glu Phe
 340 345 350

Pro Val Pro Lys Pro Met Val Thr His Gly Leu Ser His Pro Val Ala
 355 360 365

Leu Thr Phe Thr Lys Glu Asn Ser Leu Leu Val Leu Asp Thr Ala Ser
 370 375 380

His Ser Ile Lys Val Tyr Lys Val Asp Trp Gly
 385 390 395

<210> 3

<211> 3008

<212> DNA

<213> Canis sp.

<220>

<221> CDS

<222> (698)..(1897)

<223>

<220>

<221> misc_feature

<222> (2692)..(2692)

<223> N=any nucleic acid

<220>

<221> misc_feature

<222> (2748)..(2748)

<223> N=any nucleic acid

<220>

<221> misc_feature

<222> (2750)..(2750)

<223> N=any nucleic acid

<220>

<221> misc_feature

<222> (2793)..(2793)

<223> N=any nucleic acid

<220>

<221> misc_feature

<222> (2845)..(2845)

<223> N=any nucleic acid

<220>

<221> misc_feature

<222> (2916)..(2916)

<223> N=any nucleic acid

<220>
<221> misc_feature
<222> (2918)..(2918)
<223> N=any nucleic acid

<220>
<221> misc_feature
<222> (2931)..(2931)
<223> N=any nucleic acid

<220>
<221> misc_feature
<222> (2941)..(2941)
<223> N=any nucleic acid

<220>
<221> misc_feature
<222> (2990)..(2990)
<223> N=any nucleic acid

<400> 3
ccccaaaggcc ccccgggccc ccaggcaacc ccaggccccc aggcaacca aggccccccg 60
gccccaaaggcc ccccaggttc ccggccccaa gaaccaaggcc ccccgggccc ccgccccag 120
caccagcac caagcccccg ccccgggccc caagcaccca gcccagcac ccagcccccg 180
ccccagcccc agccccagca cccagcccc gcccagcac ccagccccag caccagccc 240
ccgccccagc cccagcccc gtccccccc ccagcaccca gcccagccc cagcagcagc 300
accagcagg ggactgcaaa gcgtaggcta cccaggtgg aacaccgtgt tctagttttg 360
ctttgcggtt tgcagcctgg gcgatcgggg gccaccgctc gagcctgttt cccgtcgcg 420
aaagcgggagc cgccccgccc cgcccccgcc ctgcctgaag gtcacgggccc tgggcctgcg 480
gcgcgcggtg cggcccgcga gcgtccgctc ccgcgcctc cgcagtcagc gcccgcccg 540
ccgcccgggg accgcaggcc gcggccgaga ggctgcgcgc tgcgcccgcg acgtcaggcc 600
ccgccccgcc ccgccccgcc ccgtgaccgg ccccgggccc ggccccggcc ccggcccccg 660

7/12

accgagcggc gcccgcgga gcggcggcgg ccgcgcg	atg ggg gcc gaa gcg gcg	715
	Met Gly Ala Glu Ala Ala	
	1 5	
ggg agc ggg cgg gcg ctg cgg gag ctg gtg cgc gag gcc gag gtc agc		763
Gly Ser Gly Arg Ala Leu Arg Glu Leu Val Arg Glu Ala Glu Val Ser		
	10 15 20	
ttg ctc gag tgc aag gtg tgc ttc gag agg ttc ggc cac cgc cag cag		811
Leu Leu Glu Cys Lys Val Cys Phe Glu Arg Phe Gly His Arg Gln Gln		
	25 30 35	
cgg cgc ccg cgc aac ctg ccc tgc ggc cac gtg gtg tgc ctg gcc tgc		859
Arg Arg Pro Arg Asn Leu Pro Cys Gly His Val Val Cys Leu Ala Cys		
	40 45 50	
gtg gcg gcc ctg gcg cac ccg cgg acg ctg gcc ctg gag tgc ccc ttc		907
Val Ala Ala Leu Ala His Pro Arg Thr Leu Ala Leu Glu Cys Pro Phe		
	55 60 65 70	
tgc cgc cgg gcc tgc cgc ggc tgc gac acc agc gac tgc ctg ccg gtg		955
Cys Arg Arg Ala Cys Arg Gly Cys Asp Thr Ser Asp Cys Leu Pro Val		
	75 80 85	
ctt cac ctc ctg gag ctc ctg ggc tgc gcg ctg cgc cca gcc ccc gcc		1003
Leu His Leu Leu Glu Leu Leu Gly Ser Ala Leu Arg Pro Ala Pro Ala		
	90 95 100	
gcc ccc cgc gcc gcc ccc cgc gcc gcc ccc tgc gcc ccg ggc gcc ctc		1051
Ala Pro Arg Ala Ala Pro Arg Ala Ala Pro Cys Ala Pro Gly Ala Leu		
	105 110 115	
gcc tgc cat cac gcg ttc gga ggc tgg ggg acc ctg gtc aac ccc acg		1099
Ala Cys His His Ala Phe Gly Gly Trp Gly Thr Leu Val Asn Pro Thr		
	120 125 130	
ggg ctg gcg ctg tgc ccc aag acc ggg cgg gtc gtg gtg gtg cac gac		1147
Gly Leu Ala Leu Cys Pro Lys Thr Gly Arg Val Val Val Val His Asp		
	135 140 145 150	
ggc agg agg cgg gtc aag atc ttt gac tcc ggg gga gga tgc gcc cat		1195
Gly Arg Arg Arg Val Lys Ile Phe Asp Ser Gly Gly Gly Cys Ala His		
	155 160 165	
cag ttt gga gag aag ggg gag gct gcc cag gac att agg tac ccc ctg		1243
Gln Phe Gly Glu Lys Gly Glu Ala Ala Gln Asp Ile Arg Tyr Pro Leu		
	170 175 180	
gac gtc gcc gtc acc aac gac tgc cac gtg gtt gtc acc gac gcc ggc		1291
Asp Val Ala Val Thr Asn Asp Cys His Val Val Val Thr Asp Ala Gly		
	185 190 195	
gac cgc tcc atc aaa gtg ttt gat ttc ttt ggc cag atc aag ctc gtc		1339
Asp Arg Ser Ile Lys Val Phe Asp Phe Phe Gly Gln Ile Lys Leu Val		
	200 205 210	
att gga gac cag ttt tcc tta cct tgg ggc gtg gag acc acc cct cag		1387
Ile Gly Asp Gln Phe Ser Leu Pro Trp Gly Val Glu Thr Thr Pro Gln		
	215 220 225 230	

8/12

aat ggg gtc gtg gta act gac gcc gag gca ggg tcg ctg cac ctg ctg Asn Gly Val Val Val Thr Asp Ala Glu Ala Gly Ser Leu His Leu Leu 235 240 245	1435
gaa gtc gac ttt gca gaa gga gcc ctc cag agg act gaa aag ctg caa Glu Val Asp Phe Ala Glu Gly Ala Leu Gln Arg Thr Glu Lys Leu Gln 250 255 260	1483
ggt cat ctg tgc aac ccg cga ggg gtg gcc gtg tcc tgg ctc act ggg Gly His Leu Cys Asn Pro Arg Gly Val Ala Val Ser Trp Leu Thr Gly 265 270 275	1531
gcc att gcg gtc ctg gag cac cct ccg ggg ctg ggg gct ggg gcg ggc Ala Ile Ala Val Leu Glu His Pro Pro Gly Leu Gly Ala Gly Ala Gly 280 285 290	1579
agc acc gcc gtg aag gtg ttc agc cca act atg cag ctg atc ggc cag Ser Thr Ala Val Lys Val Phe Ser Pro Thr Met Gln Leu Ile Gly Gln 295 300 305 310	1627
gtg gat acc ttt ggg ctc agc ctc ttt ttc ccc tct aga ata acc gcc Val Asp Thr Phe Gly Leu Ser Leu Phe Phe Pro Ser Arg Ile Thr Ala 315 320 325	1675
tcc gcc gtg acc ttt gat cac cag ggg aat gtg att gtt gca gat act Ser Ala Val Thr Phe Asp His Gln Gly Asn Val Ile Val Ala Asp Thr 330 335 340	1723
tct agt cag gcc gtc cta tgc ttg gga cag cct gag gaa ttt cca gtc Ser Ser Gln Ala Val Leu Cys Leu Gly Gln Pro Glu Glu Phe Pro Val 345 350 355	1771
ctg aag ccc atc atc acc cat ggt ctt tcc cat cct gtg gca ctg acc Leu Lys Pro Ile Ile Thr His Gly Leu Ser His Pro Val Ala Leu Thr 360 365 370	1819
ttc acc aag gag aat tct ctt ctt gtg ctg gac agt gca gcc cat tcc Phe Thr Lys Glu Asn Ser Leu Leu Val Leu Asp Ser Ala Ala His Ser 375 380 385 390	1867
gta aaa gtc tac aag gct gac tgg ggg taa tgggggtgtgg tgggggtcct Val Lys Val Tyr Lys Ala Asp Trp Gly 395	1917
ggaactgccca ctaatccagt ttaaccctgg atgaattaat cccatctctc gaacggggat	1977
cattataact gcctgacaga cttataaagg ttgaaggtaa ttattaaaga ataataatga	2037
agtctaccgt ttattgagtt atgtgctccc tgtgctagga aactttgcaa atattagctc	2097
agcgtgtcct tacagtggta cccagggagg taatgcccac cattaatccc attttagaga	2157
tgagaaaaact gagaccgag ggtttaagtg attctctgaa ggtcatgttt acttactgtg	2217
acagtcacaa tgggaactct attctgactc cccaatccct tgctcctaag taggataaca	2277
gatgtgagaa aacgacagca tgtgtctata tgttggttact gtgtgtactc tctttacagg	2337
tagctatttc tcttggttgg acgtgcagag aaaggagact ttctagagag ttcaagagga	2397
aaaagggtag tgtgatgagc atggacgtga gtgtcattga acttgctggg tctttgatgt	2457

cacagtaggt agaatgactg tggatccttc aactgccctt gggaaaggta aacatgtctg 2517
ttgggacctg gatgtcctcc atcataggaa cccaggaaat actagttggt tgctgcagaa 2577
aggcttgtgt ggacataagt tcaaaactac tgccgaccac cgtacattca cacacctcca 2637
gtgggagatg gctggaagac agtcctgtga caggtctgca ttcatagaac aagangccgc 2697
caccgttggt tcacggcaga atgagtttgc ctgcctcttc ataatctgtg ncnacccgaa 2757
acccttttgt gatagagttt ttctctgtgc catttnaatt tgtcccattg cacacactgt 2817
tttcccctaa ccagctccct tgatgctnag ctagcattta ggccactggt aaacccctgt 2877
atacttcttg agttgaagtt aagctttgac ccagataang nctgctttaa tacntgcagt 2937
cgantggacc gaataagggg gaaatttcag gtgaggtggc cgggttcttt atnaaccggt 2997
tttggtttgt a 3008

<210> 4
<211> 399
<212> PRT
<213> Canis sp.

<220>
<221> misc_feature
<222> (2692)..(2692)
<223> N=any nucleic acid
<220>
<221> misc_feature
<222> (2748)..(2748)
<223> N=any nucleic acid
<220>
<221> misc_feature
<222> (2750)..(2750)
<223> N=any nucleic acid
<220>
<221> misc_feature
<222> (2793)..(2793)

<223> N=any nucleic acid

<220>

<221> misc_feature

<222> (2845)..(2845)

<223> N=any nucleic acid

<220>

<221> misc_feature

<222> (2916)..(2916)

<223> N=any nucleic acid

<220>

<221> misc_feature

<222> (2918)..(2918)

<223> N=any nucleic acid

<220>

<221> misc_feature

<222> (2931)..(2931)

<223> N=any nucleic acid

<220>

<221> misc_feature

<222> (2941)..(2941)

<223> N=any nucleic acid

<220>

<221> misc_feature

<222> (2990)..(2990)

<223> N=any nucleic acid

<400> 4

Met Gly Ala Glu Ala Ala Gly Ser Gly Arg Ala Leu Arg Glu Leu Val
1 5 10 15

Arg Glu Ala Glu Val Ser Leu Leu Glu Cys Lys Val Cys Phe Glu Arg
20 25 30

Phe Gly His Arg Gln Gln Arg Arg Pro Arg Asn Leu Pro Cys Gly His
35 40 45

11/12

Val Val Cys Leu Ala Cys Val Ala Ala Leu Ala His Pro Arg Thr Leu
 50 55 60

Ala Leu Glu Cys Pro Phe Cys Arg Arg Ala Cys Arg Gly Cys Asp Thr
 65 70 75 80

Ser Asp Cys Leu Pro Val Leu His Leu Leu Glu Leu Leu Gly Ser Ala
 85 90 95

Leu Arg Pro Ala Pro Ala Ala Pro Arg Ala Ala Pro Arg Ala Ala Pro
 100 105 110

Cys Ala Pro Gly Ala Leu Ala Cys His His Ala Phe Gly Gly Trp Gly
 115 120 125

Thr Leu Val Asn Pro Thr Gly Leu Ala Leu Cys Pro Lys Thr Gly Arg
 130 135 140

Val Val Val Val His Asp Gly Arg Arg Arg Val Lys Ile Phe Asp Ser
 145 150 155 160

Gly Gly Gly Cys Ala His Gln Phe Gly Glu Lys Gly Glu Ala Ala Gln
 165 170 175

Asp Ile Arg Tyr Pro Leu Asp Val Ala Val Thr Asn Asp Cys His Val
 180 185 190

Val Val Thr Asp Ala Gly Asp Arg Ser Ile Lys Val Phe Asp Phe Phe
 195 200 205

Gly Gln Ile Lys Leu Val Ile Gly Asp Gln Phe Ser Leu Pro Trp Gly
 210 215 220

Val Glu Thr Thr Pro Gln Asn Gly Val Val Val Thr Asp Ala Glu Ala
 225 230 235 240

Gly Ser Leu His Leu Leu Glu Val Asp Phe Ala Glu Gly Ala Leu Gln
 245 250 255

Arg Thr Glu Lys Leu Gln Gly His Leu Cys Asn Pro Arg Gly Val Ala
 260 265 270

Val Ser Trp Leu Thr Gly Ala Ile Ala Val Leu Glu His Pro Pro Gly
 275 280 285

Leu Gly Ala Gly Ala Gly Ser Thr Ala Val Lys Val Phe Ser Pro Thr
290 295 300

Met Gln Leu Ile Gly Gln Val Asp Thr Phe Gly Leu Ser Leu Phe Phe
305 310 315 320

Pro Ser Arg Ile Thr Ala Ser Ala Val Thr Phe Asp His Gln Gly Asn
325 330 335

Val Ile Val Ala Asp Thr Ser Ser Gln Ala Val Leu Cys Leu Gly Gln
340 345 350

Pro Glu Glu Phe Pro Val Leu Lys Pro Ile Ile Thr His Gly Leu Ser
355 360 365

His Pro Val Ala Leu Thr Phe Thr Lys Glu Asn Ser Leu Leu Val Leu
370 375 380

Asp Ser Ala Ala His Ser Val Lys Val Tyr Lys Ala Asp Trp Gly
385 390 395

- <210> 5
- <211> 12
- <212> DNA
- <213> Canis sp.

<400> 5
gccgcccccc gc